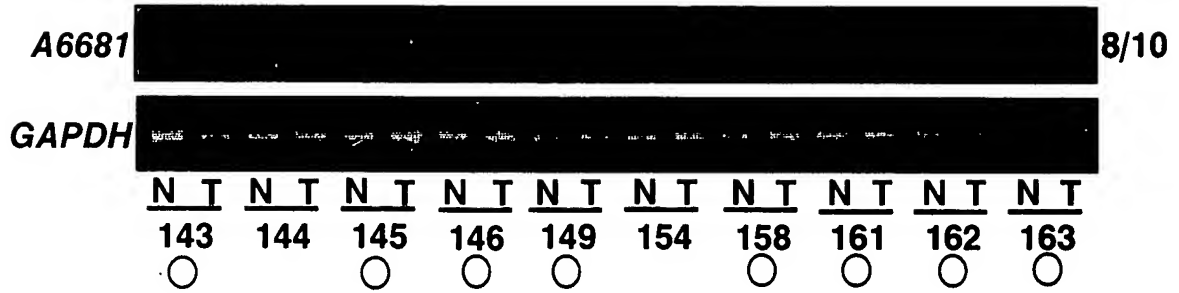| Case No.	40	53	90	143	145	148	153	154	156	159	161	177
Ratio	3.4	3.3	16	3.5	2.1	3.1	2.6	2.7	2.3	5.6	9.1	1.4

FIG.1A

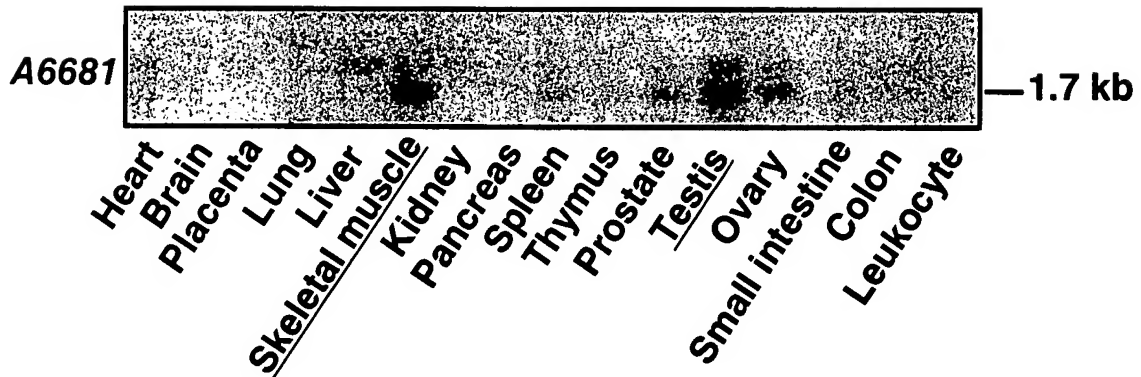FIG.1B

FIG.1C

FIG.2A

A
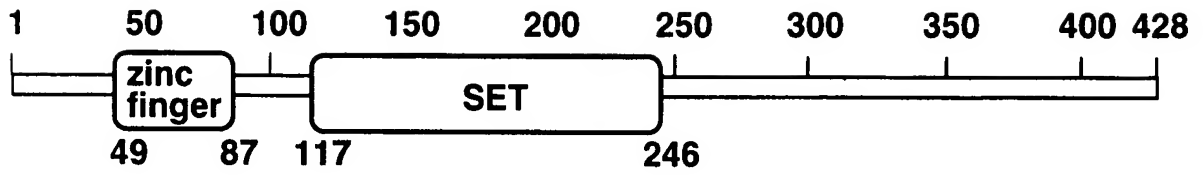
```
ZNFN3A1  :   1   MEPLKVEKFATANRGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKEKLM  60
                 ME LKVEKF TANRGNGLRAV PLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKEKLM
AK010447:   1   MEALKVEKFTTANRGNGLRAVAPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKEKLM  60
```

```
ZNFN3A1  :  61   RCSQCRVAKYCSAKCQKKAWPDHKRECKCLKSCKPRYPPDSVRLLGRVVFKLMDGAPSES  120
                 RCSQCR+AKYCSAKCQKKAWPDH+REC CLKSCKPRYPPDSVRLLGRV+ KLMD PSES          B
AK010447:  61   RCSQCRIAKYCSAKCQKKAWPDHRRECSCLKSCKPRYPPDSVRLLGRVIVKLMDEKPSES  120
```

```
ZNFN3A1  : 121   EKLYSFYDLESNINKLTEDKKEGLRQLVMTFQHFMREEIQDASQLPPAFDLFEAFAKVIC  180
                 EKLYSFYDLESNI+KLTEDKKEGLRQL MTFQHFMREEIQDASQLPP+FDLFEAFAKVIC
AK010447: 121   EKLYSFYDLESNISKLTEDKKEGLRQLAMTFQHFMREEIQDASQLPPSFDLFEAFAKVIC  180
```

```
ZNFN3A1  : 181   NSFTICNAEMQEVGVGLYPSISLLNHSCDPNCSIVFNGPHLLLRAVRDIEVGEELTICYL  240
                 NSFTICNAEMQEVGVGLYPS+SLLNHSCDPNCSIVFNGPHLL RAVR+IE GEELTICYL
AK010447: 181   NSFTICNAEMQEVGVGLYPSMSLLNHSCDPNCSIVFNGPHLLLRAVREIEAGEELTICYL  240
```

```
ZNFN3A1  : 241   DMLMTSEERRKQLRDQYCFECDCFRCQTQDKDADMLTGDEQVWKEVQESLKKIEELKAHW  300
                 DMLMTSEERRKQLRDQYCFECDC RCQTQDKDADMLTGDEQ+WKEVQESLKKIEELKAHW
AK010447: 241   DMLMTSEERRKQLRDQYCFECDCIRCQTQDKDADMLTGDEQIWKEVQESLKKIEELKAHW  300
```

```
ZNFN3A1  : 301   KWEQVLAMCQAIISSNSERLPDINIYQLKVLDCAMDACINLGLLEEALFYGTRTMEPYRI  360
                 KWEQVLA+CQAII+SNS RLPDINIYQLKVLDCAMDACINLG+LEEALFY  RTMEPYRI
AK010447: 301   KWEQVLALCQAIINSNSNRLPDINIYQLKVLDCAMDACINLGMLEEALFYAMRTMEPYRI  360
```

```
ZNFN3A1  : 361   FFPGSHPVRGVQVMKVGKLQLHQGMFPQAMKNLRLAFDIMRVTHGREHSLIEDLILLLEE  420
                 FFPGSHPVRGVQVMKVGKLQLHQGMFPQAMKNLRLAFDIM+VTHGREHSLIEDLILLLEE
AK010447: 361   FFPGSHPVRGVQVMKVGKLQLHQGMFPQAMKNLRLAFDIMKVTHGREHSLIEDLILLLEE  420
```

```
ZNFN3A1  : 421   CDANIRAS  428
                 CDANIRAS
AK010447: 421   CDANIRAS  428
```
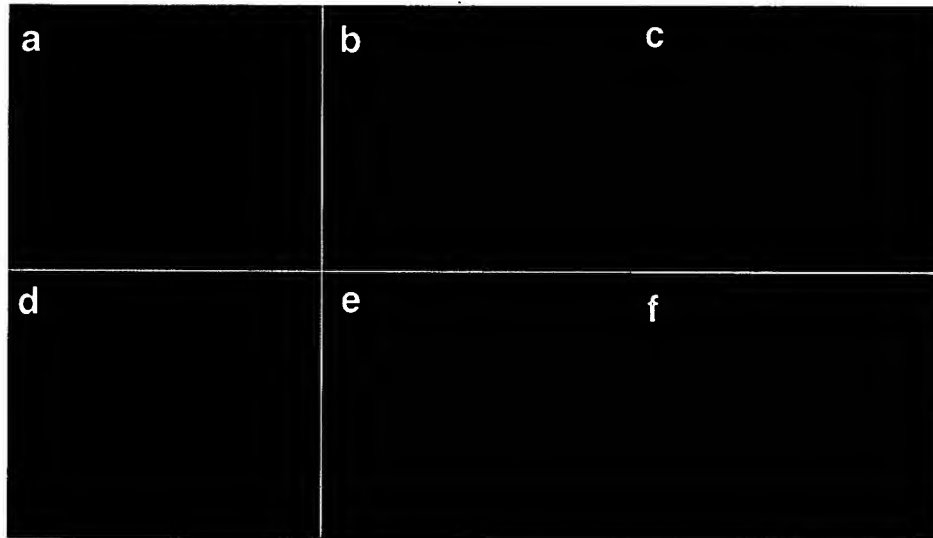
FIG.2B

FIG.3A   FIG.3B   FIG.3C

a   b   c

d   e   f
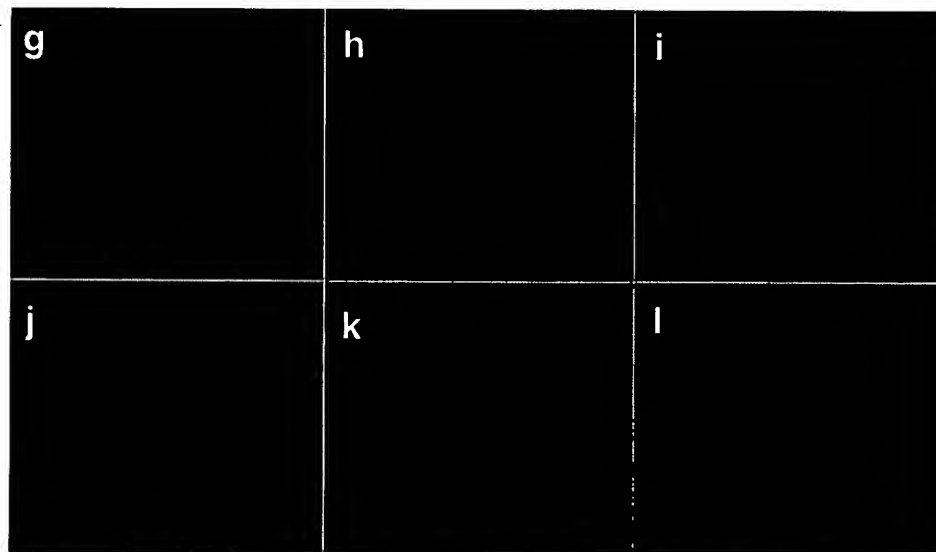
FIG.3D   FIG.3E   FIG.3F
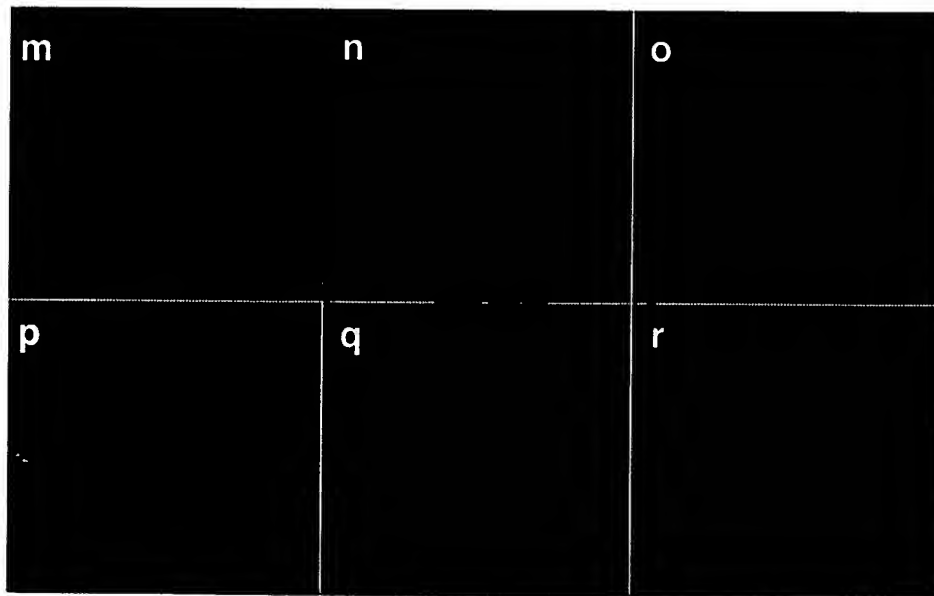
FIG.3G   FIG.3H   FIG.3I

g   h   i

j   k   l

FIG.3J   FIG.3K   FIG.3L

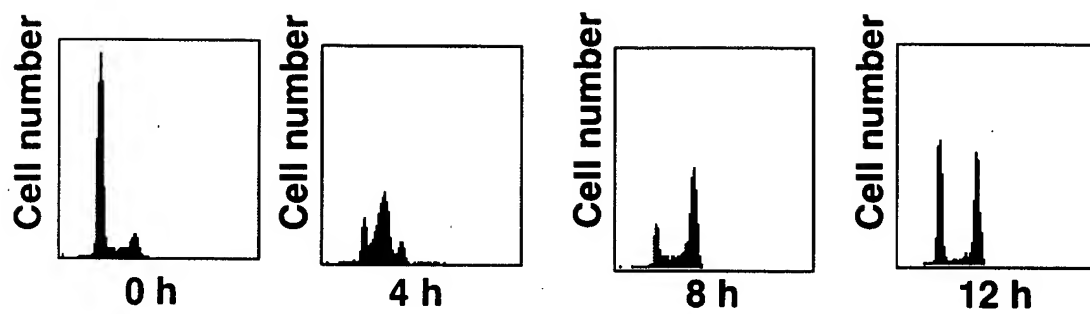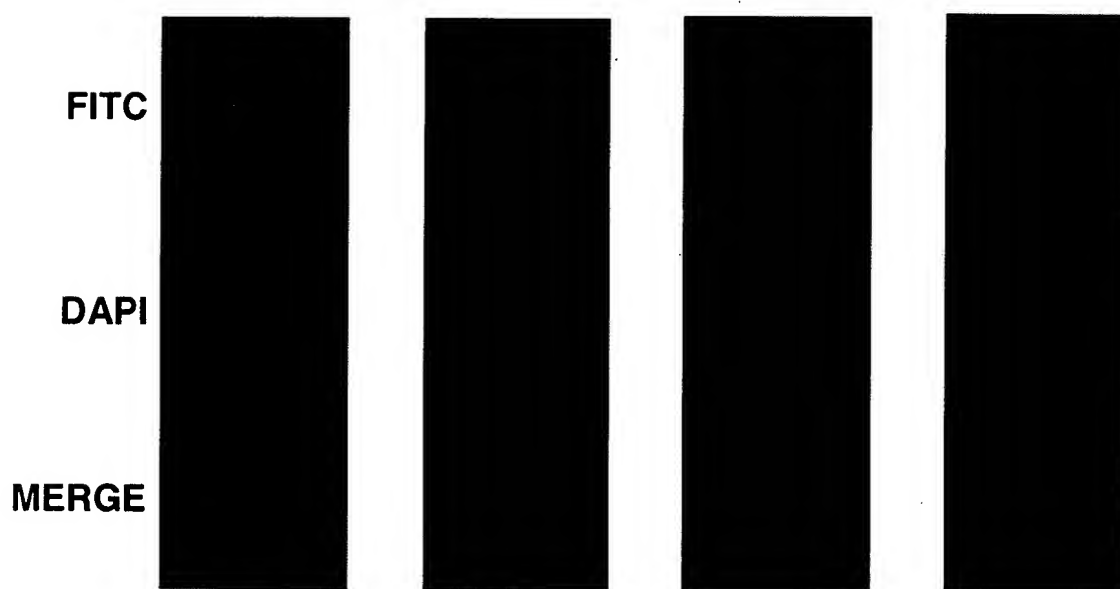FIG.3M   FIG.3N   FIG.3O
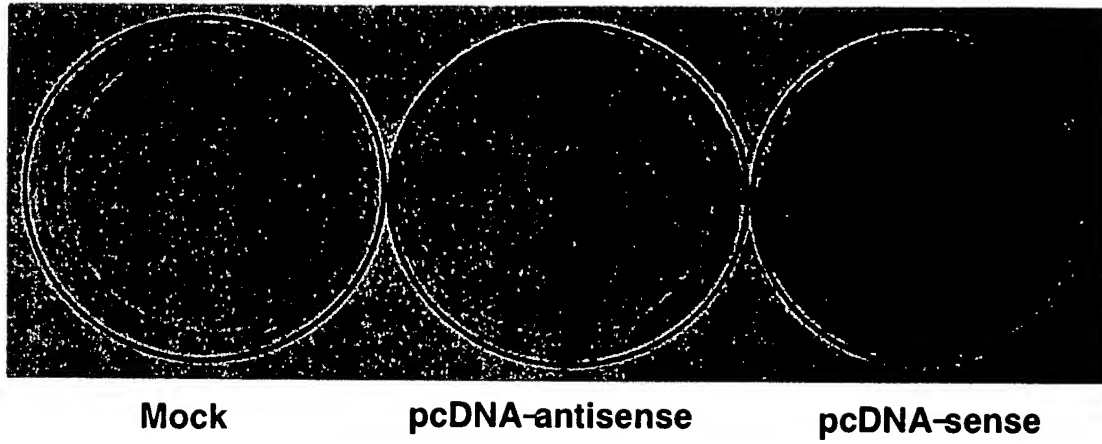

FIG.3P   FIG.3Q   FIG.3R

FIG.4A

FIG.4B

Mock   pcDNA-antisense   pcDNA-sense

FIG.5A

FIG.5B

ZNFN3A1

GAPDH

Mock NIH3T3- NIH3T3-
      antisense ZNFN3A1
      ZNFN3A1

FIG.5C

FIG.5D

-8   +1   +8

GCGGGAGG\boxed{ATG}GAGCCGCTGAAGGTGGAAA

initiation codon

⟵————— **As, Se** —————⟶
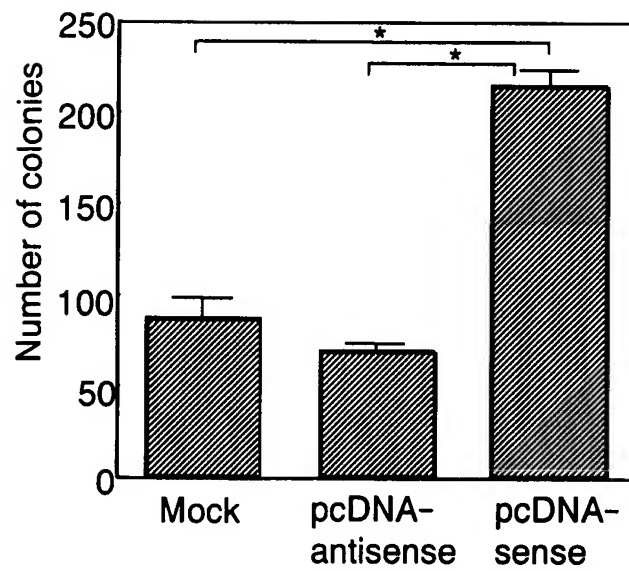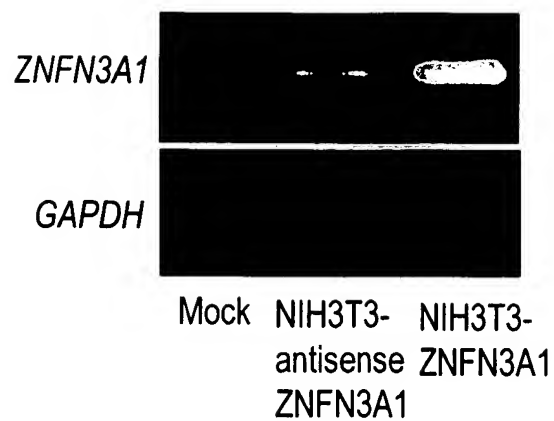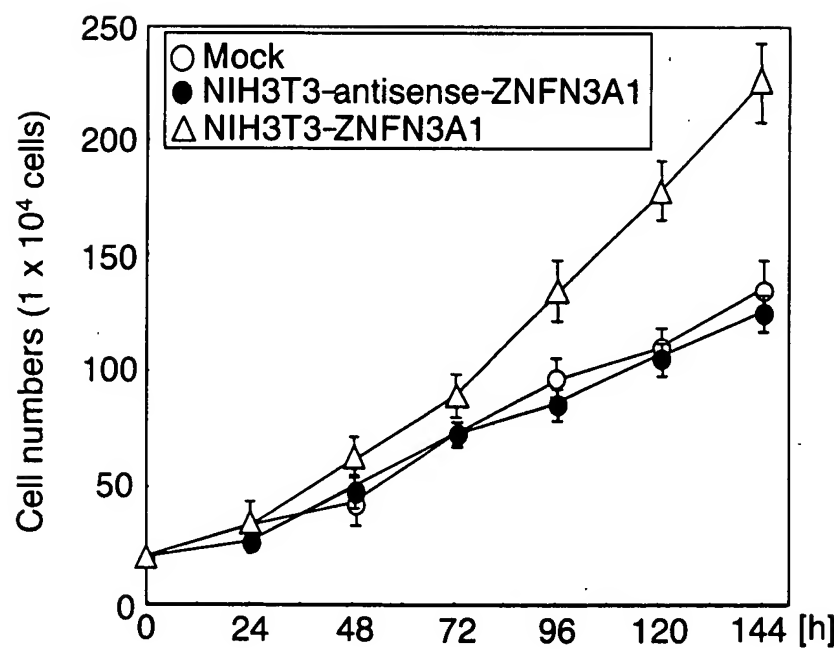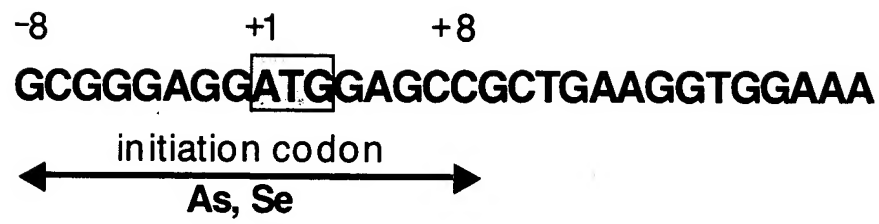
FIG.6A

FIG.6B

FIG.6C

FIG.6D

FIG.6E

FIG. 7A

Bait: pAS2-1 (empty)
Prey: pACT2-KIAA0054

Bait: pAS2-1 (ZNFN3A1)
Prey: pACT2-KIAA0054

FIG. 7B

FIG. 7C

FIG. 8

pFLAG-CMV (Mock)	—	+	+	—	—
pFLAG-CMV-ZNFN3A1	—	—	—	+	+
pCMV-HA (Mock)	—	+	—	+	—
pCMV-HA-KIAA0054 (Full)	—	—	+	—	+

Extract
(IB: anti-Pol II [N-20])

MW [kDa]

215 —
132 —
95 —

◄RNA
polymerase II

IP: anti-FLAG
IB: anti-Pol II [N-20]

MW [kDa]

215 —
132 —
95 —

◄RNA
polymerase II

IP: anti-HA
IB: anti-Pol II [N-20]

MW [kDa]

132 —
95 —

IP: anti-Pol II [N-20]
IB: anti-FLAG

42.5 —

◄ FLAG-ZNFN3A1

MW [kDa]

215 —
132 —
95 —

◄ HA-KIAA0054

IP: anti-Pol II [N-20]
IB: anti-HA

42.5 —

FIG. 9

	Experimental probability	Theoretical probability	Experimental / Theoretical
C C C T C	(37.0%)	0.015 (1.5%)	24.6
C C C T C C	(34.8%)	0.0034 (0.34%)	102.3
C C C C T C C	(20.7%)	0.00079 (0.079%)	262
C C C T C C T	(20.0%)	0.00079 (0.079%)	253

$\Downarrow$

	Experimental probability	Theoretical probability	Experimental / Theoretical
(C) C C C T C C (T)	(10.6%)	0.00018 (0.018%)	589
(A) G G A G G G (G)	(10.6%)	0.00018 (0.018%)	589

FIG. 10A
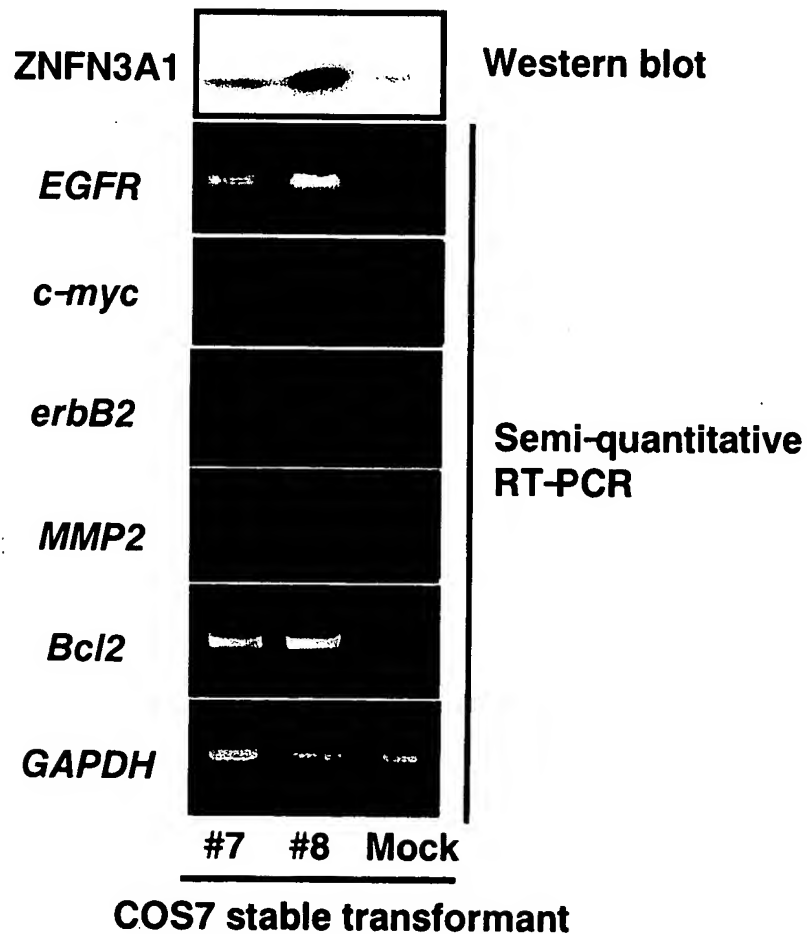
FIG. 10B
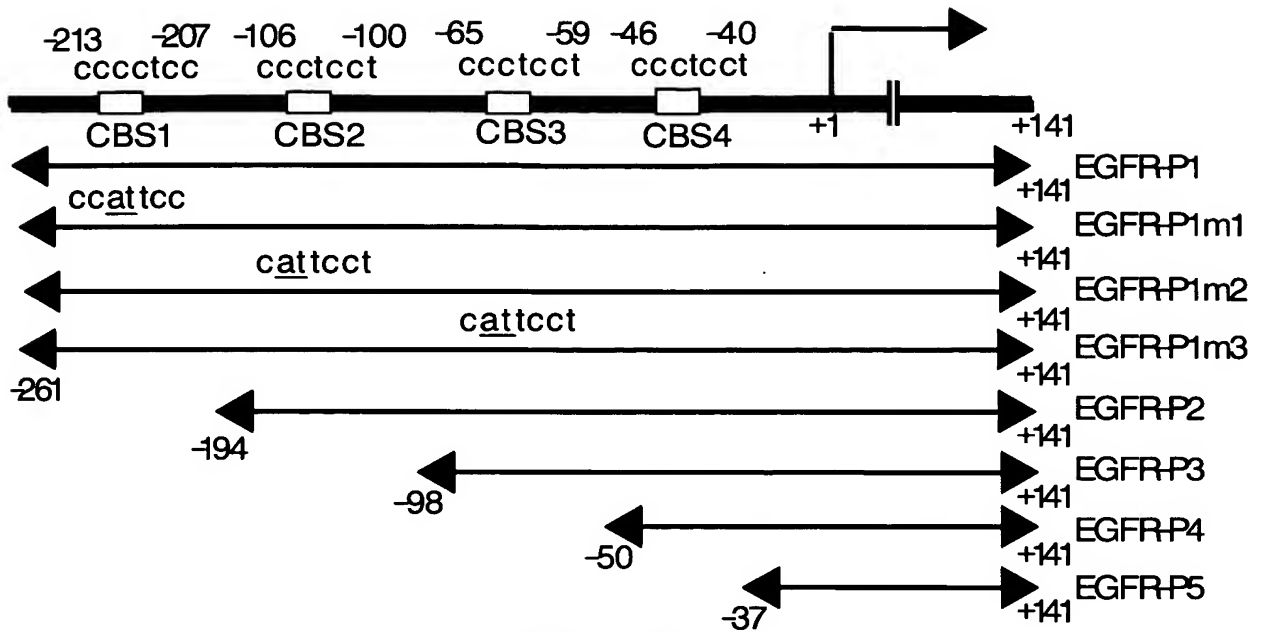
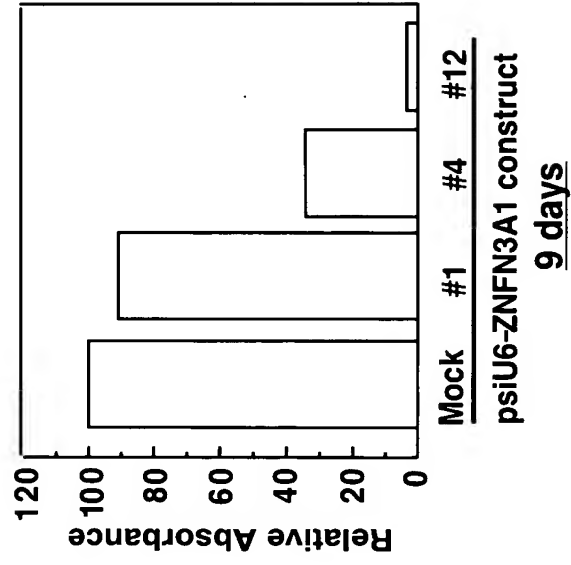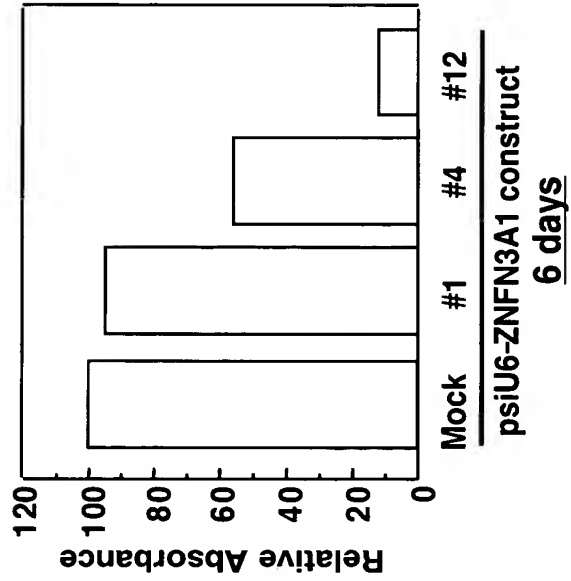**FIG. 11A**
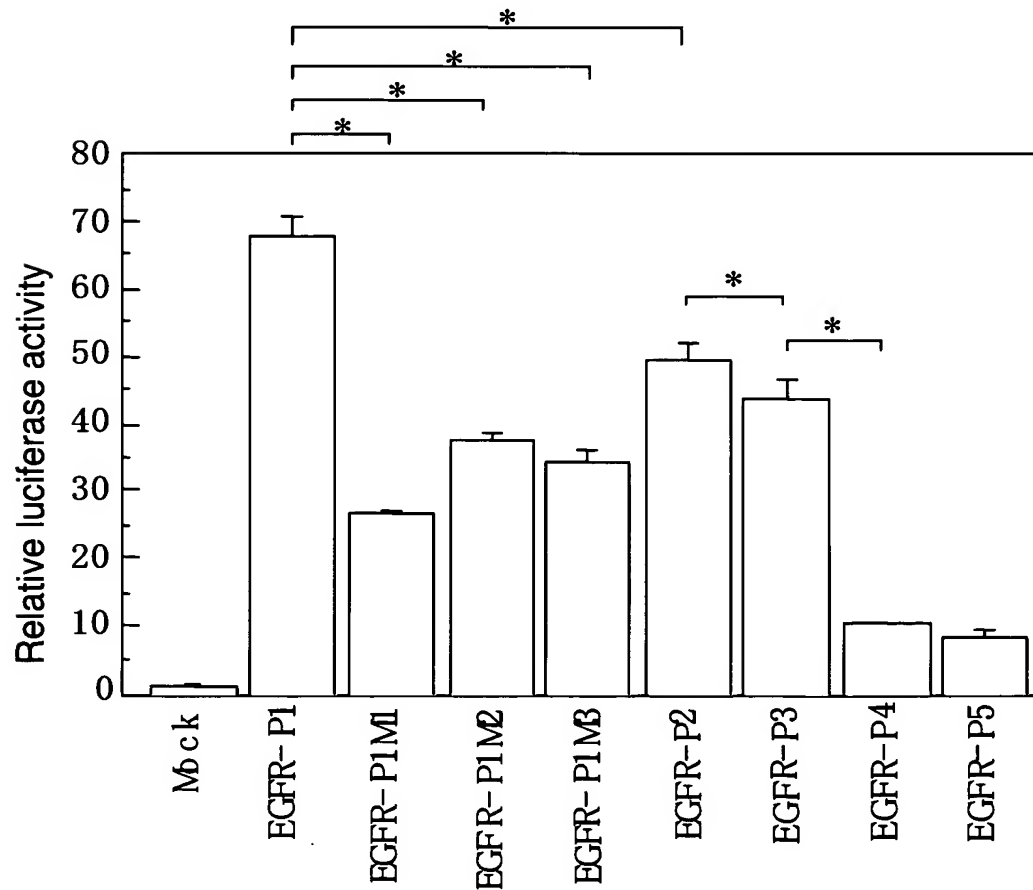
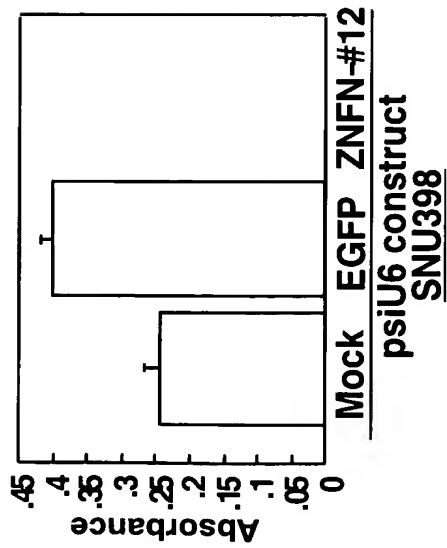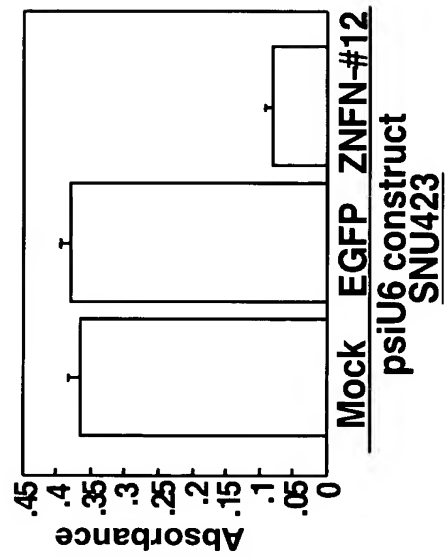**FIG. 11B**
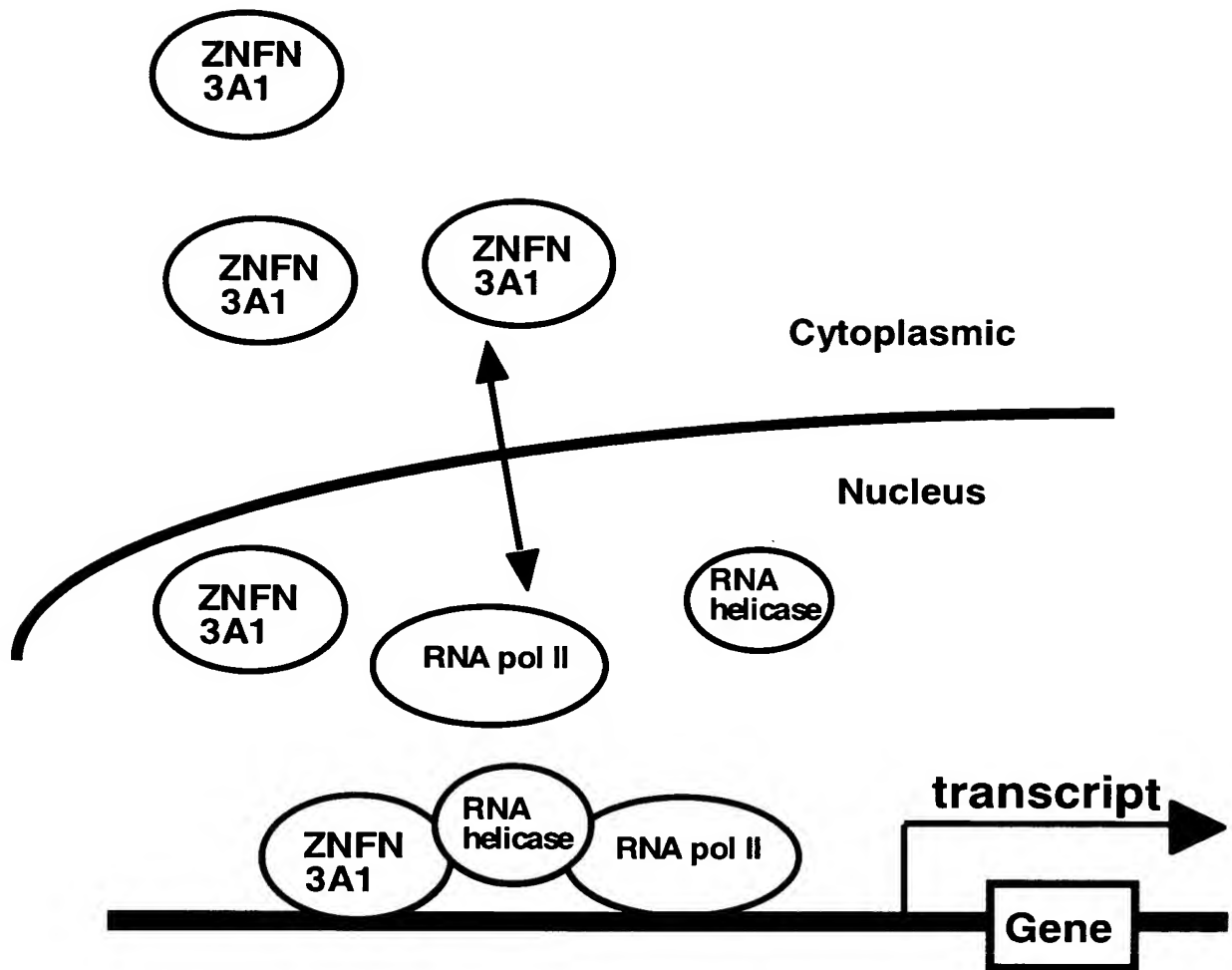
FIG. 12
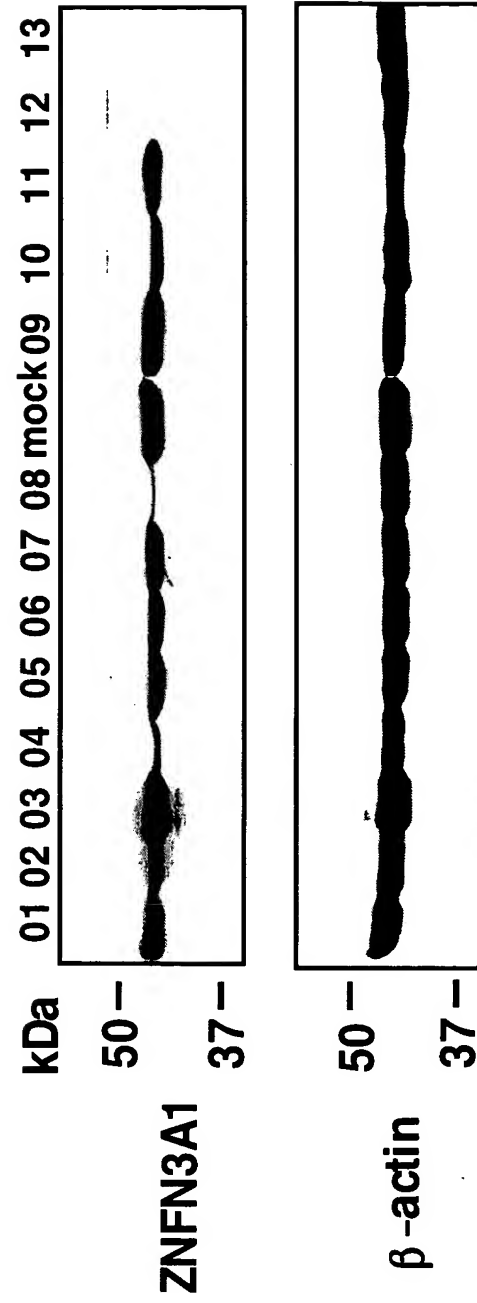
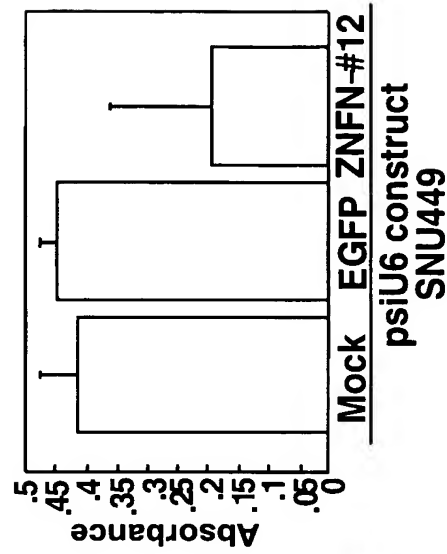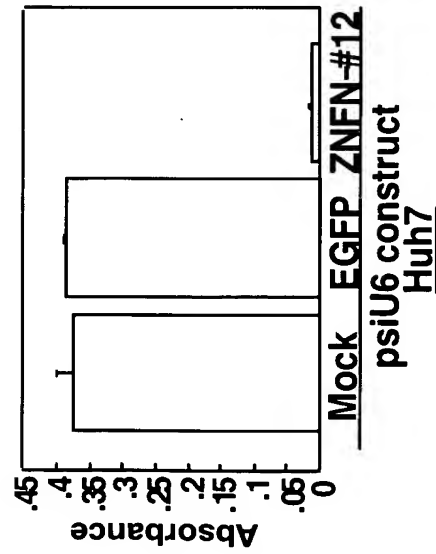FIG. 13
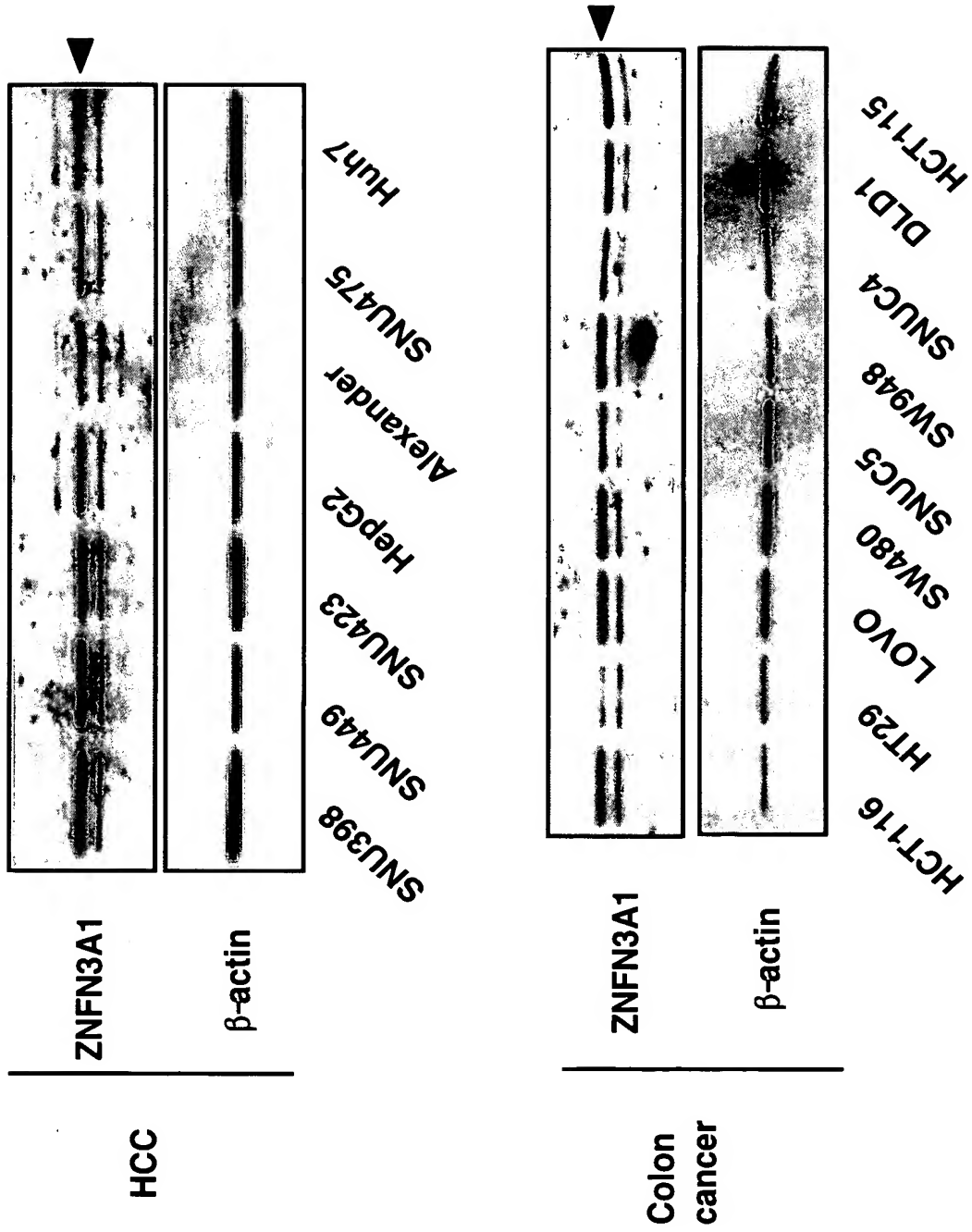
FIG. 14
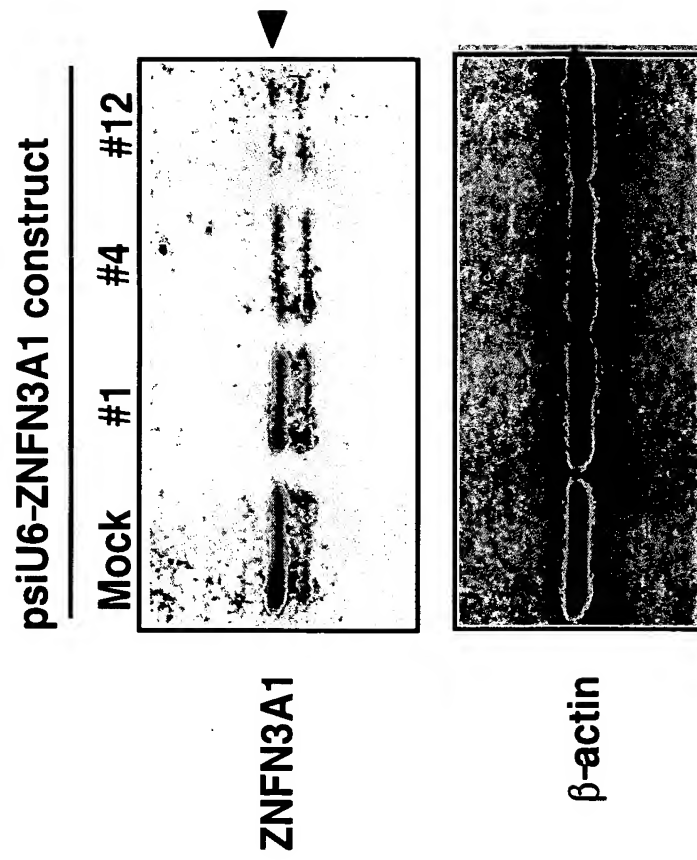
FIG. 15

FIG. 16B

FIG. 16A

FIG. 17A

FIG. 17B

FIG. 17C

FIG. 17D
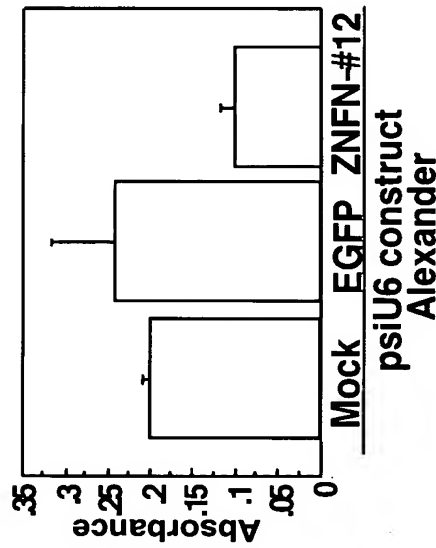
FIG. 17E
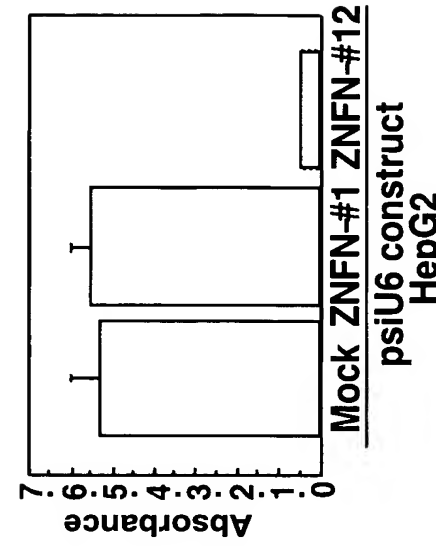
FIG. 17F
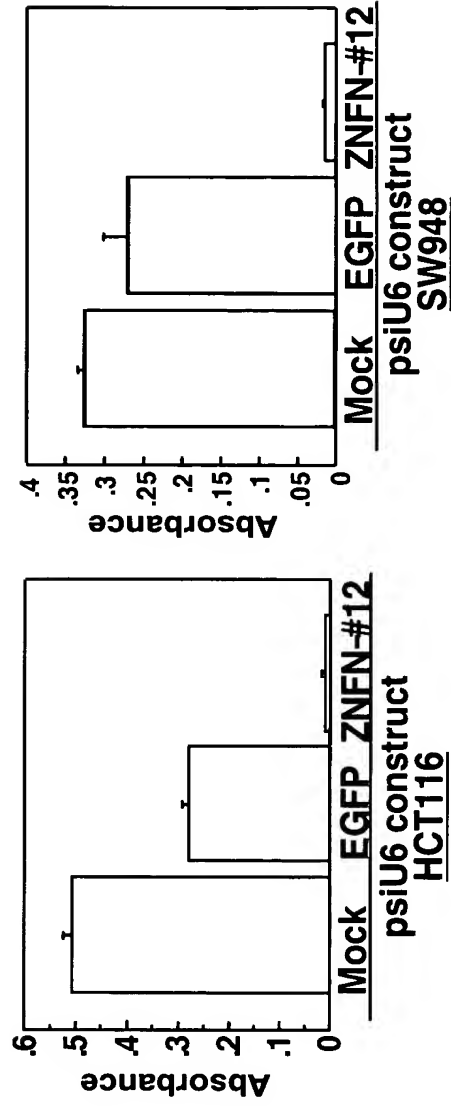
FIG. 17H

FIG. 17G
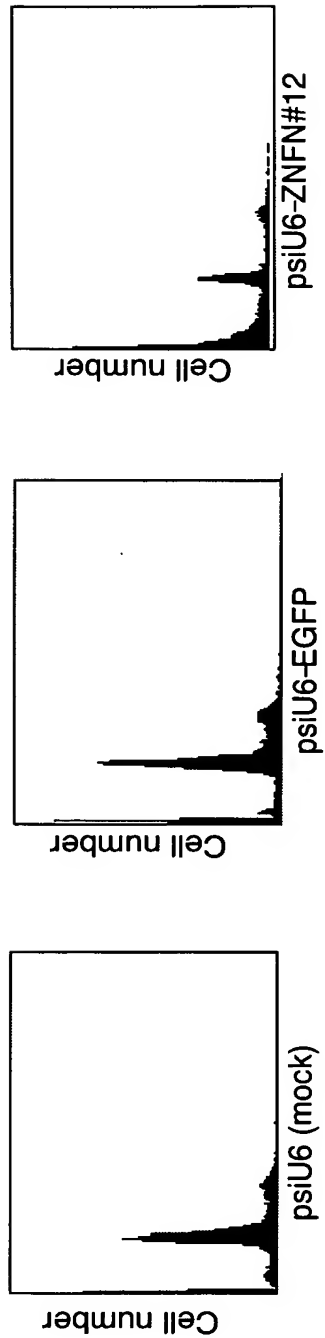
Transfected plasmids	Region (%)				
	Sub-G1	G0/G1	S	G2/M	
psiU6 (Mock)	16.01	71.18	5.07	7.15	
psiU6-EGFP	16.32	58.87	10.91	12.43	
psiU6-ZNFN#12	62.30	26.23	4.42	6.53	

FIG. 18